

Variations in the non-coding transcriptome as a driver of inter-strain divergence and physiological adaptation in bacteria

Matthias Kopf*, Stephan Klähn*, Ingeborg Scholz, Wolfgang R. Hess[§] and Björn Voß

Genetics and Experimental Bioinformatics, Faculty of Biology, University of Freiburg,
Schänzlestr. 1, 79104 Freiburg, Germany

[§]Corresponding author

*shared first authors

Supporting file S4 | Visualization of the dRNA-seq data for the plasmid pSYLC of *Synechocystis* sp. PCC 6714.

The colored graphs represent the coverage of reads from the treated libraries for ten sequenced conditions. The corresponding colors are given at the bottom of each page. The TSS positions are indicated by black arrows, e.g. at the beginning of each predicted transcriptional unit (TU, shown in red), and the read coverage graphs are highlighted for the following 100 bp. The coverage from the untreated library is shown grey. The y-axis of the graphs is square-root-scaled but the tick labels show the true normalized coverage values. Protein coding genes are shown in blue, tRNA in green and rRNA in dark grey. The data for the forward strand is shown above and data for the reverse strand below the x-axis. The x-axis shows the nucleotide position of the plasmid pSYLC in bp. This document is searchable by locus tags from *Synechocystis* sp. PCC 6714, gene names (if available), nucleotide position (every 2000 bp) and the *Synechocystis* sp. PCC 6803 locus tags of the 2854 orthologous protein-coding genes.

--- Primary-read-start threshold - - - Secondary-mean-coverage cutoff







